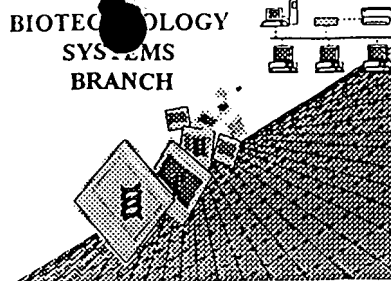# RAW SEQUENCE LISTING
ERROR REPORT

The Biotechnology Systems Branch of the Scientific and Technical Information Center (STIC) detected errors when processing the following computer readable form:

Application Serial Number: ___09/483,831___

Source: ___1600___

Date Processed by STIC: ___7/26/2001___

THE ATTACHED PRINTOUT EXPLAINS DETECTED ERRORS.
PLEASE FORWARD THIS INFORMATION TO THE APPLICANT BY EITHER:
1) INCLUDING A COPY OF THIS PRINTOUT IN YOUR NEXT COMMUNICATION TO THE APPLICANT, WITH A NOTICE TO COMPLY or,
2) TELEPHONING APPLICANT AND FAXING A COPY OF THIS PRINTOUT, WITH A NOTICE TO COMPLY
FOR CRF SUBMISSION QUESTIONS, PLEASE CONTACT MARK SPENCER, 703-308-4212.

FOR SEQUENCE RULES INTERPRETATION, PLEASE CONTACT ROBERT WAX, 703-308-4216.
PATENTIN 2.1 e-mail help: patin21help@uspto.gov or phone 703-306-4119 (R. Wax)
PATENTIN 3.0 e-mail help: patin3help@uspto.gov or phone 703-306-4119 (R. Wax)

TO REDUCE ERRORED SEQUENCE LISTINGS, PLEASE USE THE CHECKER VERSION 3.0 PROGRAM, ACCESSIBLE THROUGH THE U.S. PATENT AND TRADEMARK OFFICE WEBSITE. SEE BELOW:

Checker Version 3.0

The Checker Version 3.0 application is a state-of the-art Windows based software program employing a logical and intuitive user-interface to check whether a sequence listing is in compliance with format and content rules. Checker Version 3.0 works for sequence listings generated for the original version of 37 CFR §§1.821 – 1.825 effective October 1, 1990 (old rules) and the revised version (new rules) effective July 1, 1998 as well as World Intellectual Property Organization (WIPO) Standard ST.25.
Checker Version 3.0 replaces the previous DOS-based version of Checker, and is Y2K-compliant. Checker allows public users to check sequence listings in Computer Readable form (CRF) before submitting them to the United States Patent and Trademark Office (USPTO).
Use of Checker prior to filing the sequence listing is expected to result in fewer errored sequence listings, thus saving time and money.

Checker Version 3.0 can be down loaded from the USPTO website at the following address:
http://www.uspto.gov/web/offices/pac/checker

RAW SEQUENCE LISTING   DATE: 07/26/2001
PATENT APPLICATION: US/09/483,831   TIME: 08:17:26

Input Set : **A:\20264149.app**
Output Set: **N:\CRF3\07262001\I483831.raw**

SEQUENCE LISTING
```
  9 (1) GENERAL INFORMATION:
 11      (i) APPLICANT: UNITED STATES OF AMERICA; DEPT.
 12                    OF HEALTH AND HUMAN SERVICES
 14     (ii) TITLE OF INVENTION: MOTILITY STIMULATING
 15                       PROTEIN USEFUL IN CANCER DIAGNOSIS AND
 16                       THERAPY
 18    (iii) NUMBER OF SEQUENCES: 69
 20     (iv) CORRESPONDENCE ADDRESS:
 21          (A) ADDRESSEE: MORGAN & FINNEGAN
 22          (B) STREET: 345 PARK AVENUE
 23          (C) CITY: NEW YORK
 24          (D) STATE: NEW YORK
 25          (E) COUNTRY: U.S.A.
 26          (F) ZIP: 10154
 28      (v) COMPUTER READABLE FORM:
 29          (A) MEDIUM TYPE: Floppy Disk
 30          (B) COMPUTER: IBM PC compatible
 31          (C) OPERATING SYSTEM: PC-DOS/MS-DOS
 32          (D) SOFTWARE: WordPerfect 5.1
 34     (vi) CURRENT APPLICATION DATA:
```
C--> 35   **(A) APPLICATION NUMBER: US/09/483,831**
C--> 36   **(B) FILING DATE: 17-Jan-2000**
```
 37          (C) CLASSIFICATION:
```
C--> 47   **(vii) PRIOR APPLICATION DATA:**
```
 40          (A) APPLICATION NUMBER: 08/346,455
 41          (B) FILING DATE: 28-NOV-1994
 44          (A) APPLICATION NUMBER: 08/249,182
 45          (B) FILING DATE: 25-MAY-1994
 48          (A) APPLICATION NUMBER: 07/822,043
 49          (B) FILING DATE: 17-JAN-1992
 51   (viii) ATTORNEY/AGENT INFORMATION:
 52          (A) NAME: DOROTHY R. AUTH
 58          (B) REGISTRATION NUMBER: 36,434
```
C--> 59   **(C) REFERENCE/DOCKET NUMBER: 2026-4149US3**
```
 61     (ix) TELECOMMUNICATION INFORMATION:
 63          (B) TELEFAX: (212) 751-6849
```

**Does Not Comply
Corrected Diskette Needed**

ERRORED SEQUENCES
```
2295 (2) INFORMATION FOR SEQ ID NO: 67:
2297      (i) SEQUENCE CHARACTERISTICS:
2298          (A) LENGTH: 861
2299          (B) TYPE: amino acid
2300          (C) STRANDEDNESS: single
2301          (D) TOPOLOGY: Unknown
```

```
2303      (ii) MOLECULE TYPE: protein
2305     (iii) HYPOTHETICAL: No
2307      (ix) FEATURE:
2308           (A) NAME/KEY: N-tera 2D1 ATX protein
2309           (B) LOCATION:
2310           (C) IDENTIFICATION METHOD:
2311           (D) OTHER INFORMATION:
2314      (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 67:
2316 Met Ala Arg Arg Ser Ser Phe Gln Ser Cys Gln Ile Ile Ser Leu Phe
2317   1               5                  10                  15
2318 Thr Phe Ala Val Gly Val Asn Ile Cys Leu Gly Phe Thr Ala His Arg
2319             20                  25                  30
2320 Ile Lys Arg Ala Glu Gly Trp Glu Glu Gly Pro Pro Thr Val Leu Ser
2321         35                  40                  45
2322 Asp Ser Pro Trp Thr Asn Ile Ser Gly Ser Cys Lys Gly Arg Cys Phe
2323      50                  55                  60
2324 Glu Leu Gln Glu Ala Gly Pro Pro Asp Cys Arg Cys Asp Asn Leu Cys
2325 65                  70                  75                  80
2326 Lys Ser Tyr Thr Ser Cys Cys His Asp Phe Asp Glu Leu Cys Leu Lys
2327             85                  90                  95
2328 Thr Ala Arg Ala Trp Glu Cys Thr Lys Asp Arg Cys Gly Glu Val Arg
2329             100                 105                 110
2330 Asn Glu Glu Asn Ala Cys His Cys Ser Glu Asp Cys Leu Ala Arg Gly
2331             115                 120                 125
2332 Asp Cys Cys Thr Asn Tyr Gln Val Val Cys Lys Gly Glu Ser His Trp
2333      130                 135                 140
2334 Val Asp Asp Asp Cys Glu Glu Ile Lys Ala Ala Glu Cys Pro Ala Gly
2335 145                 150                 155                 160
2336 Phe Val Arg Pro Pro Leu Ile Ile Phe Ser Val Asp Gly Phe Arg Ala
2337             165                 170                 175
2343 Ser Tyr Met Lys Lys Gly Ser Lys Val Met Pro Asn Ile Glu Lys Leu
2344             180                 185                 190
2345 Arg Ser Cys Gly Thr His Ser Pro His Met Arg Pro Val Tyr Pro Thr
2346             195                 200                 205
2347 Lys Thr Phe Pro Asn Leu Tyr Thr Leu Ala Thr Gly Leu Tyr Pro Glu
2348      210                 215                 220
2350 Ser His Gly Ile Val Gly Asn Ser Met Tyr Asp Pro Val Phe Asp Ala
2351 225                 230                 235                 240
2352 Thr Phe His Leu Arg Gly Arg Glu Lys Phe Asn His Arg Trp Trp Gly
2353             245                 250                 255
2354 Gly Gln Pro Leu Trp Ile Thr Ala Thr Lys Gln Arg Gly Glu Ser Trp
2355             260                 265                 270
2356 Asn Ile Leu Leu Val Cys Cys His Pro Ser Arg Ala Glu Ile Leu Thr
2357             275                 280                 285
2358 Ile Leu Gln Trp Leu Thr Leu Pro Asp His Glu Arg Leu Arg Ser Met
2359         290                 295                 300
2361 Pro Ser Ile Leu Ser Asn Leu Ile Ser Leu Asp Thr Asn Met Pro Phe
2362 305                 310                 315                 320
2363 Gly Pro Glu Met Thr Asn Pro Leu Arg Glu Ile Asp Lys Ile Val Gly
```

```
2364                   325                330                335
2365 Gln Leu Met Asp Gly Leu Lys Gln Leu Lys Leu His Arg Cys Val Asn
2366              340                345                350
2367 Val Ile Phe Val Gly Asp His Gly Met Glu Asp Val Thr Cys Asp Arg
2368              355                360                365
2369 Thr Glu Phe Leu Ser Asn Tyr Leu Thr Asn Val Asp Asp Ile Thr Leu
2370      370                375                380
2372 Val Pro Gly Thr Leu Gly Ile Arg Ser Lys Phe Ser Asn Asn Ala Lys
2373 .385                390                395                400
2374 Tyr Asp Pro Lys Ala Ile Ile Ala Asn Leu Thr Cys Lys Lys Pro Asp
2375              405                410                415
2376 Gln His Phe Lys Pro Tyr Leu Lys Gln His Leu Pro Lys Arg Leu His
2377              420                425                430
2378 Tyr Ala Asn Asn Arg Arg Ile Glu Asp Ile His Leu Leu Val Glu Arg
2379              435                440                445
2380 Arg Trp His Val Ala Arg Lys Pro Leu Asp Val Tyr Lys Lys Pro Ser
2381      450                455                460
2383 Gly Lys Cys Phe Phe Gln Gly Asp His Gly Phe Asp Asn Lys Val Asn
2384 465                470                475                480
2385 Ser Met Gln Thr Val Phe Val Gly Tyr Gly Pro Thr Phe Lys Tyr Lys
2386      .          485                490                495
2387 Thr Lys Val Pro Pro Phe Glu Asn Ile Glu Leu Tyr Asn Val Met Cys
2388              500                505                510
2389 Asp Leu Leu Gly Leu Lys Pro Ala Pro Asn Asn Gly Thr His Gly Ser
2390              515                520                525
2391 Leu Asn His Leu Leu Arg Thr Asn Thr Phe Arg Pro Thr Met Pro Glu
2392      530                535                540
2399 Glu Val Thr Arg Pro Asn Tyr Pro Gly Ile Met Tyr Leu Gln Ser Asp
2400 445                450                555                560
2401 Phe Asp Leu Gly Cys Thr Cys Asp Asp Lys Val Glu Pro Lys Asn Lys
2402              565                570                575
2403 Leu Asp Glu Leu Asn Lys Arg Leu His Thr Lys Gly Ser Thr Glu Glu
2404              580                585                590
2405 Arg His Leu Leu Tyr Gly Arg Pro Ala Val Leu Tyr Arg Thr Arg Tyr
2406      .595                600                605
2407 Asp Val Leu Tyr His Thr Asp Phe Glu Ser Gly Tyr Ser Glu Ile Phe
2408      610                615                620
2410 Leu Met Pro Leu Trp Thr Ser Tyr Thr Val Ser Lys Gln Ala Glu Val
2411 625                630                635                640
2412 Ser Ser Val Pro Asp His Leu Thr Ser Cys Val Arg Pro Asp Val Arg
2413              645                650                655
2414 Val Ser Pro Ser Phe Ser Gln Asn Cys Leu Ala Tyr Lys Asn Asp Lys
2415              660                665                670
2416 Gln Met Ser Tyr Gly Phe Leu Phe Pro Pro Tyr Leu Ser Ser Ser Pro
2417              675                680                685
2418 Glu Ala Lys Tyr Asp Ala Phe Leu Val Thr Asn Met Val Pro Met Tyr
2419      690                695                700
2421 Pro Ala Phe Lys Arg Val Trp Asn Tyr Phe Gln Arg Val Leu Val Lys
2422 705                710                715                720
```

E--> 2400 (445)   (450)   ──────555   560

numbering of amino acid must be sequential,

```
2423 Lys Tyr Ala Ser Glu Arg Asn Gly Val Asn Val Ile Ser Gly Pro Ile
2424             725                 730             735
2425 Phe Asp Tyr Asp Tyr Asp Gly Leu His Asp Thr Glu Asp Lys Ile Lys
2426             740                 745             750
2427 Gln Tyr Val Glu Gly Ser Ser Ile Pro Val Pro Thr His Tyr Tyr Ser
2428         755                 760             765
2429 Ile Ile Thr Ser Cys Leu Asp Phe Thr Gln Pro Ala Asp Lys Cys Asp
2430     770                 775             780
2432 Gly Pro Leu Ser Val Ser Ser Phe Ile Leu Arg His Arg Pro Asp Asn
2433 785                 790             795                 800
2434 Glu Glu Ser Cys Asn Ser Ser Glu Asp Glu Ser Lys Trp Val Glu Glu
2435             805                 810             815
2436 Leu Met Lys Met His Thr Ala Arg Val Arg Asp Ile Glu His Leu Thr
2437             820                 825             830
2438 Ser Leu Asp Phe Phe Arg Lys Thr Ser Arg Ser Tyr Pro Glu Ile Leu
2439             835                 840             845
2440 Thr Leu Lys Thr Tyr Leu His Thr Tyr Glu Ser Glu Ile
2441     850                 855             860
2564 (2) INFORMATION FOR SEQ ID NO: 69:
2565     (i) SEQUENCE CHARACTERISTICS:
2566         (A) LENGTH: 915
2567         (B) TYPE: amino acid
2568         (C) STRANDEDNESS: single
2569         (D) TOPOLOGY: Unknown
2571     (ii) MOLECULE TYPE: cDNA
2573     (iii) HYPOTHETICAL: No
2575     (ix) FEATURE:
2576         (A) NAME/KEY: A2058 ATX protein
2577         (B) LOCATION:
2578         (C) IDENTIFICATION METHOD:
2579         (D) OTHER INFORMATION:
2581     (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 69:
2583 Met Ala Arg Arg Ser Ser Phe Gln Ser Cys Gln Ile
2584   1             5                 10
2585 Ile Ser Leu Phe Thr Phe Ala Val Gly Val Ser Ile
2586             15                 20
2587 Cys Leu Gly Phe Thr Ala His Arg Ile Lys Arg Ala
2588   25                 30                 35
2589 Glu Gly Trp Glu Glu Gly Pro Pro Thr Val Leu Ser
2590             40                 45
2591 Asp Ser Pro Trp Thr Asn Ile Ser Gly Ser Cys Lys
2592       50                 55                 60
2593 Gly Arg Cys Phe Glu Leu Gln Glu Ala Gly Pro Pro
2594             65                 70
2595 Asp Cys Arg Cys Asp Asn Leu Cys Lys Ser Tyr Thr
2596             75                 80
2597 Ser Cys Cys His Asp Phe Asp Glu Leu Cys Leu Lys
2598   85                 90                 95
2599 Thr Ala Arg Gly Trp Glu Cys Thr Lys Asp Arg Cys
```

```
2600              100                   105
2606 Gly Glu Val Arg Asn Glu Glu Asn Ala Cys His Cys
2607      110                   115                   120
2608 Ser Glu Asp Cys Leu Ala Arg Gly Asp Cys Cys Thr
2609              125                   130
2610 Asn Tyr Gln Val Val Cys Lys Gly Glu Ser His Trp
2611      135                   140
2612 Val Asp Asp Asp Cys Glu Glu Ile Lys Ala Ala Glu
2613 145              150                   155
2614 Cys Pro Ala Gly Phe Val Arg Pro Pro Leu Ile Ile
2615              160                   165
2616 Phe Ser Val Asp Gly Phe Arg Ala Ser Tyr Met Lys
2617      170                   175                   180
2618 Lys Gly Ser Lys Val Met Pro Asn Ile Glu Lys Leu
2619              185                   190
2620 Arg Ser Cys Gly Thr His Ser Pro Tyr Met Arg Pro
2621      195                   200
2622 Val Tyr Pro Thr Lys Thr Phe Pro Asn Leu Tyr Thr
2623 205              210                   215
2624 Leu Ala Thr Gly Leu Tyr Pro Glu Ser His Gly Ile
2625              220                   225
2626 Val Gly Asn Ser Met Tyr Asp Pro Val Phe Asp Ala
2627      230                   235                   240
2628 Thr Phe His Leu Arg Gly Arg Glu Lys Phe Asn His
2629              245                   250
2630 Arg Trp Trp Gly Gly Gln Pro Leu Trp Ile Thr Ala
2631      255                   260
2632 Thr Lys Gln Gly Val Lys Ala Gly Thr Phe Phe Trp
2633 265              270                   275
2634 Ser Val Val Ile Pro His Glu Arg Arg Ile Leu Thr
2635              280                   285
2636 Ile Leu Arg Trp Leu Thr Leu Pro Asp His Glu Arg
2637      290                   295                   300
2638 Pro Ser Val Tyr Ala Phe Tyr Ser Glu Gln Pro Asp
2639              305                   310
2640 Phe Ser Gly His Lys Tyr Gly Pro Phe Gly Pro Glu
2641      315                   320
2642 Glu Ser Ser Tyr Gly Ser Pro Phe Thr Pro Ala Lys
2643 325              330                   335
2644 Arg Pro Lys Arg Lys Val Ala Pro Lys Arg Arg Gln
2645              340                   345
2646 Glu Arg Pro Val Ala Pro Pro Lys Lys Arg Arg Arg
2647      350                   355                   360
2648 Lys Ile His Arg Met Asp His Tyr Ala Ala Glu Thr
2649              365                   370
2650 Arg Gln Asp Lys Met Thr Asn Pro Leu Arg Glu Ile
2651      375                   380
2657 Asp Lys Ile Val Gly Gln Leu Met Asp Gly Leu Lys
2658 385              390                   395
```

Input Set : **A:\20264149.app**
Output Set: **N:\CRF3\07262001\I483831.raw**

```
2659 Gln Leu Lys Leu Arg Arg Cys Val Asn Val Ile Phe
2660         400                 405
2661 Val Gly Asp His Gly Met Glu Asp Val Thr Cys Asp
2662     410             415             420
2663 Arg Thr Glu Phe Leu Ser Asn Tyr Leu Thr Asn Val
2664             425             430
2665 Asp Asp Ile Thr Leu Val Pro Gly Thr Leu Gly Arg
2666         435             440
2667 Ile Arg Ser Lys Phe Ser Asn Asn Ala Lys Tyr Asp
2668 445             450             455
2669 Pro Lys Ala Ile Ile Ala Asn Leu Thr Cys Lys Lys
2670         460             465
2671 Pro Asp Gln His Phe Lys Pro Tyr Leu Lys Gln His
2672     470             475             480
2673 Leu Pro Lys Arg Leu His Tyr Ala Asn Asn Arg Arg
2674             485             490
2675 Ile Glu Asp Ile His Leu Leu Val Glu Arg Arg Trp
2676         495             500
2677 His Val Ala Arg Lys Pro Leu Asp Val Tyr Lys Lys
2678 505             510             515
2679 Pro Ser Gly Lys Cys Phe Phe Gln Gly Asp His Gly
2680         520             525
2681 Phe Asp Asn Lys Val Asn Ser Met Gln Thr Val Phe
2682     530             535             540
2683 Val Gly Tyr Gly Pro Thr Phe Lys Tyr Lys Thr Lys
2684             545             550
2685 Val Pro Pro Phe Glu Asn Ile Glu Leu Tyr Asn Val
2686         555             560
2687 Met Cys Asp Leu Leu Gly Leu Lys Pro Ala Pro Asn
2688 565             570             575
2689 Asn Gly Thr His Gly Ser Leu Asn His Leu Leu Arg
2690         580             585
2691 Thr Asn Thr Phe Arg Pro Thr Met Pro Glu Glu Val
2692     590             595             600
2693 Thr Arg Pro Asn Tyr Pro Gly Ile Met Tyr Leu Gln
2694             605             610
2695 Ser Asp Phe Asp Leu Gly Cys Thr Cys Asp Asp Lys
2696         615             620
2697 Val Glu Pro Lys Asn Lys Leu Asp Glu Leu Asn Lys
2698 625             630             635
2699 Arg Leu His Thr Lys Gly Ser Thr Glu Glu Arg His
2700         640             645
2701 Leu Leu Tyr Gly Arg Pro Ala Val Leu Tyr Arg Thr
2702     650             655             660
2708 Arg Tyr Asp Ile Leu Tyr His Thr Asp Phe Glu Ser
2709             665             670
2710 Gly Tyr Ser Glu Ile Phe Leu Met Leu Leu Trp Thr
2711         675             680
2712 Ser Tyr Thr Val Ser Lys Gln Ala Glu Val Ser Ser
```

```
2713 685                    690                    695
2714 Val Pro Asp His Leu Thr Ser Cys Val Arg Pro Asp
2715             700                    705
2716 Val Arg Val Ser Pro Ser Phe Ser Gln Asn Cys Leu
2717     710                    715                720
2718 Ala Tyr Lys Asn Asp Lys Gln Met Ser Tyr Gly Phe
2719                     725                730
2720 Leu Phe Pro Pro Tyr Leu Ser Ser Ser Pro Glu Ala
2721         735                    740
2722 Lys Tyr Asp Ala Phe Leu Val Thr Asn Met Val Pro
2723 745                     750                    755
2724 Met Tyr Pro Ala Phe Lys Arg Val Trp Asn Tyr Phe
2725                 760                765
2726 Gln Arg Val Leu Val Lys Lys Tyr Ala Ser Glu Arg
2727     770                    775                    780
2728 Asn Gly Val Asn Val Ile Ser Gly Pro Ile Phe Asp
2729                     785                790
2730 Tyr Asp Tyr Asp Gly Leu His Asp Thr Glu Asp Lys
2731         795                    800
2732 Ile Lys Gln Tyr Val Glu Gly Ser Ser Ile Pro Val
2733 805                     810                    815
2734 Pro Thr His Tyr Tyr Ser Ile Ile Thr Ser Cys Leu
2735                 820                825
2736 Asp Phe Thr Gln Pro Ala Asp Lys Cys Asp Gly Pro
2737     830                    835                    840
2738 Leu Ser Val Ser Ser Phe Ile Leu Pro His Arg Pro
2739                     845                850
2740 Asp Asn Glu Glu Ser Cys Asn Ser Ser Glu Asp Glu
2741         855                    860
2742 Ser Lys Trp Val Glu Glu Leu Met Lys Met His Thr
2743 865                     870                    875
2744 Ala Arg Val Arg Asp Ile Glu His Leu Thr Ser Leu
2745             880                    885
2746 Asp Phe Phe Arg Lys Thr Ser Arg Ser Tyr Pro Glu
2747     890                    895                    900
2748 Ile Leu Thr Leu Lys Thr Tyr Leu His Thr Tyr
2749                     905                910
2750 Glu Ser Glu Ile
E--> 2751            916
```

amino acid numbering must be placed under every 5th amino acid. 916 should be changed to 915 and placed under last amino acid (Ile).

VERIFICATION SUMMARY
PATENT APPLICATION: **US/09/483,831**

DATE: 07/26/2001
TIME: 08:17:28

Input Set : **A:\20264149.app**
Output Set: **N:\CRF3\07262001\I483831.raw**

```
L:35   M:220 C: Keyword misspelled or invalid format, [(A) APPLICATION NUMBER:]
L:36   M:220 C: Keyword misspelled or invalid format, [(B) FILING DATE:]
L:39   M:220 C: Keyword misspelled or invalid format, [(vii) PRIOR APPLICATION DATA:]
L:43   M:220 C: Keyword misspelled or invalid format, [(vii) PRIOR APPLICATION DATA:]
L:47   M:220 C: Keyword misspelled or invalid format, [(vii) PRIOR APPLICATION DATA:]
L:59   M:220 C: Keyword misspelled or invalid format, [(C) REFERENCE/DOCKET NUMBER:]
L:526  M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:31
L:1376 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:38
L:1382 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:38
L:1384 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:38
L:1388 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:38
L:1390 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:38
L:1392 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:38
L:1394 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:38
L:1396 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:38
L:1408 M:246 W: Invalid value of Alpha Sequence Header Field, [MOLECULE TYPE:], SeqNo=39
L:1460 M:246 W: Invalid value of Alpha Sequence Header Field, [MOLECULE TYPE:], SeqNo=41
L:1490 M:246 W: Invalid value of Alpha Sequence Header Field, [MOLECULE TYPE:], SeqNo=42
L:1515 M:246 W: Invalid value of Alpha Sequence Header Field, [MOLECULE TYPE:], SeqNo=43
L:1533 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:43
L:1545 M:246 W: Invalid value of Alpha Sequence Header Field, [MOLECULE TYPE:], SeqNo=44
L:1570 M:246 W: Invalid value of Alpha Sequence Header Field, [MOLECULE TYPE:], SeqNo=45
L:1600 M:246 W: Invalid value of Alpha Sequence Header Field, [MOLECULE TYPE:], SeqNo=46
L:1630 M:246 W: Invalid value of Alpha Sequence Header Field, [MOLECULE TYPE:], SeqNo=47
L:1655 M:246 W: Invalid value of Alpha Sequence Header Field, [MOLECULE TYPE:], SeqNo=48
L:1686 M:246 W: Invalid value of Alpha Sequence Header Field, [MOLECULE TYPE:], SeqNo=49
L:1711 M:246 W: Invalid value of Alpha Sequence Header Field, [MOLECULE TYPE:], SeqNo=50
L:1741 M:246 W: Invalid value of Alpha Sequence Header Field, [MOLECULE TYPE:], SeqNo=51
L:1766 M:246 W: Invalid value of Alpha Sequence Header Field, [MOLECULE TYPE:], SeqNo=52
L:1798 M:246 W: Invalid value of Alpha Sequence Header Field, [MOLECULE TYPE:], SeqNo=53
L:1843 M:246 W: Invalid value of Alpha Sequence Header Field, [MOLECULE TYPE:], SeqNo=54
L:2400 M:332 E: (32) Invalid/Missing Amino Acid Numbering, SEQ ID:67
L:2751 M:332 E: (32) Invalid/Missing Amino Acid Numbering, SEQ ID:69
```